ABSTRACT

An iterative process to associate patterns embedded in the profiles of biological signals, including gene expression profile, protein profiles, with certain cellular status, functional stages and response to permutations. The biological signals, including gene expression profile, are converted into frequency domains using wavelet transform or other frequency transforms at different scales after rearranging the order of genes. These biological signals in the frequency domain are associated with certain cellular status, functional stages and response to permutation with neural network learning. An error rate is used to determine the optimal combination of wavelet function, scale and gene order. The information enriched gene group can be extracted from the frequency domain as well.